

**Claims**

1. A method for the identification of suitable fragmentation sites in a reporter protein, wherein the reporter protein is detectable when active, the method comprising the steps of:
- (a) providing a DNA sequence encoding for said reporter protein;
  - (b) creating a library based on the DNA sequence as defined in (a),
    - wherein each individual of said library comprises a randomly created first subsequence of the DNA sequence as defined in (a), encoding for a first subdomain of said reporter protein, and
    - wherein each individual of said library comprises a randomly created complementary second subsequence of the DNA sequence as defined in (a), encoding for a complementary second subdomain of said reporter protein;
  - (c) screening and/or selection for restoration of detectable activity of said reporter protein, when said first subdomain and said complementary second subdomain are brought into close proximity;
  - (d) identifying said first subdomain and/or said first subsequence, and said complementary second subdomain and/or said complementary second subsequence, that lead to restoration of detectable activity of said reporter protein.
2. A method according to claim 1, wherein the reporter protein is detectable in vivo and/or in vitro, both as full length protein and when actively resembled by a first

subdomain and a complementary second subdomain, by a means chosen from the group consisting of color assays and growth assays.

- 5     3.     A method according to one of claims 1 or 2, wherein individuals of the library as defined in (b) are either prokaryotic or eukaryotic host cells, comprising:
- both said first subsequence and said complementary second subsequence in one and the same expression vector, suitable for (co-)expression of said first subsequence and said complementary second subsequence in vivo; or
  - said first subsequence in a first expression vector suitable for (co-)expression of said first subsequence, and said complementary second subsequence in a second expression vector suitable for (co-)expression of said complementary second subsequence.
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- 20     4.     A method according to one of claims 1 to 3, wherein screening for restoration of detectable activity of said reporter protein, when said first subdomain and said complementary second subdomain are brought into close proximity as defined in (c), comprises the following steps:
- creating a first fusion subsequence comprising the first subsequence of said reporter protein as defined in (b), fused to an oligonucleotide encoding for a first protein or peptide,
  - creating a second fusion subsequence comprising the complementary second subsequence of said reporter protein as defined in (b), fused to an oligonucleotide encoding for a second protein or peptide,
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wherein said first protein or peptide and said second protein or peptide are known to interact.

5. A method according to one of claims 1 to 4, wherein said  
5 first protein or peptide and said second protein or peptide align to each other in an anti-parallel coiled coil orientation.
6. A method according to claim 5, wherein said first protein  
10 or peptide and said second protein or peptide are leucine zippers.
7. A method according to one of claims 4 to 6, wherein said  
15 first fusion subsequence and said second subsequence are created by blunt end ligation.
8. A method according to claim 7, wherein said first fusion  
subsequence and said second fusion subsequence each comprise  
20 - a linker sequence in between said first subsequence (or said second subsequence, respectively) and said oligonucleotide encoding for a first protein or peptide (or said oligonucleotide encoding for a second protein or peptide, respectively);  
25 - at least one tag that allows for verification of the transcription of said first fusion subsequence and said second fusion subsequence.
9. A method according to one of claims 4 to 8, wherein an  
30 oligonucleotide is inserted by homologous recombination in between said first subsequence and said second subsequence, encoding for:

- a transcription terminating sequence for terminating transcription of said first or said second subsequence;
- a transcription promoting sequence for initiating transcription of said second or said first subsequence, respectively;
- a marker sequence allowing for control of successful homologous recombination.

10 10. A method according to one of claims 1 to 9, comprising the steps of:

- creating fragmentation sites in TRP1 using gene cleavage with a unique restriction enzyme RE1 and circularization;
- isolating fragments corresponding to the wild-type length;
- sub-cloning using blunt ends preferably into a pRS316 based yeast expression vector under the control of a copper promoter (pCUB1) and transforming into E. coli, preferably XL1blue;
- recombining and amplifying homologues with a unique restriction site RE2, preferably AvrII, introduced between the original N- and C-termini to allow subsequent linerization of the vector;
- locating two leucine zippers in the plasmid at the 3'- and the 5'-ends of the newly generated N- and C-termini, the zippers being positive and negative charged helices to allow heterodimerization, preferably each heterodimer containing a buried asparagine residue in a position to force antiparallel orientation of the zippers.

11. A recombinant DNA sequence for use in securing expression in a prokaryotic or eukaryotic host cell of a polypeptide product having the primary structural conformation of a first subdomain of a reporter protein or a complementary second subdomain of a reporter protein, wherein detect-  
5 able activity of said reporter protein is restored, when said first subdomain and said complementary second subdomain are brought into close proximity, and wherein said first and said complementary second subdomain are not  
10 subdomains of one of the group of proteins consisting of transcriptional activators, ubiquitin, dihydrofolate reductase,  $\beta$ -lactamase, green fluorescent protein,  $\beta$ -galactosidase, inteins, cAMP cyclase, glycinamide ribonucleotide transformylase, aminoglycoside phosphotransferase, hygromycin B phosphotransferase, luciferase.  
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12. A recombinant DNA sequence according to claim 11, wherein said DNA sequence encodes for a subdomain of a  $(\beta/\alpha)_8$ -barrel enzyme.  
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13. A recombinant DNA sequence according to one of claims 11 to 12, wherein said DNA sequence is selected from the group consisting of:  
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- (a) the DNA sequences set out in Tables ? and ? or their complementary strands;
  - (b) DNA sequences which hybridize under stringent conditions to the protein coding regions of the DNA sequences defined in (a) or fragments thereof;
  - (c) DNA sequences which, but for the degeneracy of the  
30 genetic code, would hybridize to the DNA sequences defined in (a) or (b) and which sequences code for a polypeptide having the same amino acid sequence.

14. A recombinant DNA sequence according to one of claims 11 to 13, wherein said DNA sequence is for use in securing expression in a prokaryotic or eukaryotic host cell of a polypeptide fusion product.

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15. A first subdomain of a reporter protein and/or a complementary second subdomain of a reporter protein, wherein detectable activity of said reporter protein is restored, when said first subdomain and said complementary second subdomain are brought into close proximity, and wherein said first and said complementary second subdomain are not subdomains of one of the group of proteins consisting of transcriptional activators, ubiquitin, dihydrofolate reductase,  $\beta$ -lactamase, green fluorescent protein,  $\beta$ -galactosidase, inteins, cAMP cyclase, glycinamide ribonucleotide transformylase, aminoglycoside phosphotransferase, hygromycin B phosphotransferase, luciferase.

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16. A first subdomain of a reporter protein or a complementary second subdomain of a reporter protein according to claim 15, wherein the site of fragmentation of said reporter protein into a first subdomain and a complementary second subdomain is identified by a method according to one of claims 1 to 15.

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17. A first subdomain of a reporter protein or a complementary second subdomain of a reporter protein according to one of claims 15 to 16, produced by a method of culturing a host transformed with a recombinant DNA molecule selected from the group consisting of the DNA molecules of claims 15 to 16, wherein said molecules further comprises an expression control sequence, said expression control sequence being operatively linked to said molecule.

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18. A fusion protein comprising a first subdomain of a re-  
porter protein or a complementary second subdomain of a  
5 reporter protein according to one of claims 15 to 17, and  
a further peptide or protein connected thereto in a natu-  
rally not occurring combination.
19. A prokaryotic or eukaryotic host cell line, transformed  
10 with a recombinant DNA sequence according to one of  
claims 11 to 14.
20. A host cell line according to claim 19, wherein the host  
cell line allows for homologous recombination of DNA.
- 15 21. A host cell line according to claim 20, which host cell  
line comprises a yeast cell line.
22. A host cell line according to claim 21, which yeast cell  
20 line is chosen from the group consisting of *Saccharomyces  
cerevisiae* and *Schizosaccharomyces pombe*.
23. A kit of parts, comprising a first and a second DNA-based  
expression vector, wherein
- 25 - said first expression vector contains an expression  
cassette encoding for a polypeptide product having at  
least a substantial part of the primary structural  
confirmation of a first subdomain of a reporter pro-  
tein; and
- 30 - said second expression vector contains an expression  
cassette encoding for a polypeptide product having at  
least a substantial part of the primary structural

confirmation of a complementary second subdomain of a reporter protein; and  
wherein detectable activity of said reporter protein is restored, when said first subdomain and said complementary second subdomain are brought into close proximity, and wherein said first and said complementary second subdomain are not subdomains of one the group of proteins consisting of transcriptional activators, ubiquitin, dihydrofolate reductase,  $\beta$ -lactamase, green fluorescent protein,  $\beta$ -galactosidase, inteins, cAMP cyclase, glycylamide ribonucleotide transformylase, aminoglycoside phosphotransferase, hygromycin B phosphotransferase, luciferase.

24. A kit of parts according to claim 23, further comprising a suitable prokaryotic or eukaryotic host cell line for expression of said first and second expression vector.

25. A method for detecting an interaction between a first test peptide or protein or a fragment thereof, and a second test peptide or protein or a fragment thereof, the method comprising the steps of:

- providing recombinant DNA sequences according to one of claims 11 to 14 for use in securing expression of a first subdomain of a reporter protein and a complementary second subdomain of a reporter protein;
- fusing an oligonucleotide or a gene encoding for a first test peptide or protein to the DNA sequence encoding for said first subdomain of the reporter protein, thereby creating a first DNA fusion sequence encoding for a fusion protein comprising said first subdomain of the reporter protein and said first test peptide or protein;



- fusing an oligonucleotide or a gene encoding for a second test peptide or protein to the DNA sequence encoding for said complementary second subdomain of the reporter protein, thereby creating a second DNA fusion sequence encoding for a fusion protein comprising said complementary second subdomain of the reporter protein and said second test peptide or protein;
- (co-)expressing said fusion protein comprising said first subdomain of the reporter protein and said first test peptide or protein, and said fusion protein comprising said second complementary subdomain of the reporter protein and said second test peptide or protein in a suitable prokaryotic or eukaryotic host cell;
- screening and/or selecting for restoration of detectable activity of said reporter protein.

26. A method according to claim 25, wherein a library of oligonucleotides or DNA encoding for a set of first test peptides or proteins and/or a library of oligonucleotides or DNA encoding for a set of second test peptides or proteins are fused to said first subdomain of said reporter protein and/or said complementary second subdomain of said reporter protein, respectively.

27. A method according to one of claims 25 to 26, wherein said first test peptide or protein or a fragment thereof, and said second test peptide or protein or a fragment thereof, are peptides or proteins naturally occurring in compartments chosen from the group consisting of cellular membranes, the cytosol, the mitochondrion, the peroxisome and the lumen of the secretory path.

28. A method according to one of claims 25 to 27, wherein said interaction between a first test peptide or protein or a fragment thereof and a second test peptide or protein or fragment thereof is mediated by a chemical inducer of dimerization, which binds either covalently or non-covalently to both said test peptides or proteins or fragments thereof.

29. A method for detecting the interruption of an interaction between a first test peptide or protein or a fragment thereof, and a second test peptide or protein or a fragment thereof, the method comprising the steps of:
- providing recombinant DNA sequences according to one of claims 11 to 14 for use in securing expression of a first subdomain of a reporter protein and a complementary second subdomain of a reporter protein;
  - fusing an oligonucleotide or a gene encoding for a first test peptide or protein to the DNA sequence encoding for said first subdomain of the reporter protein, thereby creating a first DNA fusion sequence encoding for a fusion protein comprising said first subdomain of the reporter protein and said first test peptide or protein;
  - fusing an oligonucleotide or a gene encoding for a second test peptide or protein to the DNA sequence encoding for said complementary second subdomain of the reporter protein, thereby creating a second DNA fusion sequence encoding for a fusion protein comprising said complementary second subdomain of the reporter protein and said second test peptide or protein;

- (co-)expressing said fusion protein comprising said first subdomain of the reporter protein and said first test peptide or protein, and said fusion protein comprising said second complementary subdomain of the reporter protein and said second test peptide or protein in a suitable prokaryotic or eukaryotic host cell;
- screening and/or selecting for interruption of interaction of said first subdomain and said second subdomain under the influence of one or more test agents.

30. Use of random circular permutation of a gene and/or the expressed polypeptide derived thereof for the identification of fragmentation sites in a reporter protein for use in a two-hybrid system.

31. Use of a host cell line that allows for homologous recombination of DNA for the generation of a recombinant DNA molecule that secures for expression of both a polypeptide product comprising a first subdomain of a reporter protein and a complementary second subdomain of a reporter protein from said recombinant DNA molecule.